

REMARKS

Applicants submit that the DNA sequence of Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) in Figure 13A contain a typographical error between nucleotide positions 1169 and 1171. The corresponding amino acid sequence of Pfu DNA polymerase D141A/E143A / V93R (SEQ ID NO: 44) and PFU DNA polymerase D141A/E143A/ V93E (SEQ ID NO: 46) is shown in Figure 13B as the following sequence ---SYTGG--- (underlining denotes amino acid position 387) which is identical to the amino acid sequence of wild type Pfu DNA polymerase in Figure 20. The presence of Glycine at position 387 is therefore consistent with the sequence GGT between nucleotide positions 1169 and 1171 not the sequence CCN as shown in the originally filed Figure 13A. Hence, the Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) sequence in Figure 13A are amended to show the wild type sequence 'GGT' instead of 'CCN' between nucleotide positions 1159 and 1161. No new matter is added.

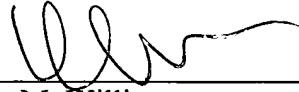
Applicants submit that the DNA sequence encoding Sac7d- Taq fusion protein (SEQ ID NO: 128) in Figure 20 contains typographical errors between nucleotide positions 230 and 232, 343 and 351, and 778 and 780.

Applicants submit that the sequence 'OTC' between positions 142 and 144 within the Taq DNA polymerase sequence and the corresponding amino acid 'X' in Figures 17B, 17C, 17U, 17V, 17NN, 17OO and 17FFF are typographical errors. The wild type DNA sequence at this location is 'GTC' and the corresponding amino acid is Valine as reported in SEQ ID NO:1 of U.S. Patent No. 5,466,591 (Abramson et al., filed February 23 1993) which is incorporated by reference on page 3, line 4 of the present application. Hence the Taq DNA polymerase nucleotide (SEQ ID NO:65) and amino acid (SEQ ID NO: 66) sequences in Figures 17B, 17C, 17U, 17V, 17NN, 17OO and 17FFF are corrected to show the wild type sequence 'GTC' and the corresponding amino acid 'Valine' between positions 142 and 144.

Applicants submit that the amendments of the figures are only made to correct typographical errors and to introduce SEQ ID Nos next to the corresponding nucleotide and amino acid sequences depicted in the Figures and that these amendments do not introduce any new matter.

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Respectfully submitted,



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Amendments to the Drawings:

Applicants further propose amendments to Figures 10, 13 A-B, 14, 17A-17S, 17T-17LL, 17MM-17DDD, 17EEE-17RRR, 18, 19 and 20 herein attached.



FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [6]5)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: [7]6)

V93R#1

5'-gAACATCCCCAAGATAgACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [8]7)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: [9]8)

V93N#1

5'-gAACATCCCCAAGATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [10]9)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: [11]10)

V93H#1

5'-gAACATCCCCAAGATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [12]11)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: [13]12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [14]13)

V93K#1

5'-gAACATCCCCAAGATAACCCCACTATTAgAg-3' (SEQ ID NO: [15]14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: [16]15)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCCCCCACTATTAgAgAAAAAg-(SEQ ID NO: [17]16)

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCCACTATTAgAgAAAAAg-3'(SEQ ID NO: [18]17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [19]18)

Cysteine

QCM#4 5'-

(Phosphate)gAACATCCCCAAGATATACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [20]19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: [21]20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [22]21)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAGATCCTCCCCTACTATTAgAgAAAAAg-3' (SEQ ID NO: [23]22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAGATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAGATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAGATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAGATTggCCCCTACTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

MARKED UP VERSION OF AMENDED FIGURE 13A

Please replace Figure 13A with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13A.

FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTCACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX] NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
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CCCATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
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GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCCTAG 2328
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PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 30)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX] NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
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GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
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AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
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GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TG TAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX] NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTT 780
TATCATGTAA TAACAAGGAC AATAAAATCT CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCCT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA [CC N] GGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGGAAGAAAG 1560
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GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAATAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGA AATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
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CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTTCAC 2040
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GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCCTAG 2328

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V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCCTCG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGAC[XXX] NNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCTTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780

TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCTTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCCG	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
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GGCTTCTACA	AACGCGGCTT	CTTCGTACAG	AAGAAGAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAACTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCCAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA	2325	

Vent DNA POLYMERASE

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTTTAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCCTCATT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAACGTGTA	GAGTGCTCGA	TGCAGTGAAG	GTCAGGAAAA	AATTTTTTGGG	AAGGGAAGTT	240
GAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGAC [XXX]	<u>NNNC</u>	CAGCTATGCG	GGGCAAAATA 300
AGGGAACATC	CAGCTGTGGT	TGACATTTAC	GAATATGACA	TACCCTTTGC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	660
AAACGGGCAG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAAACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAAC TTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAAC TTA	CCTGGGAGGA	TATGTAAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAAATATCA	TTTATTTTGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
GTATCCCCAG	ATACCC TTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTAT TCCCT	CCATACTCGG	GGACTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGC AAAAG	GGCTAT TAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500

GGGTATCCTA	AGGCAAGATG	GTA	CTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATA	AAGAGAA	ATAGAGGAAA	AGTTCGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTAT	GCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTAAA	1680
AAGAAAGCCA	AGGAATTCCT	AAACT	TACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
GAGTATGAGG	GCTTTTACTT	GAGAG	GATTCT	TTTGTTCACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACA	AGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAG	GTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGAT	GTTGTA	GAGAAAAATAG	CAAAATACAG	GGTTCCACTT	1980
GAAAAGCTTG	TTATCCATGA	GCAG	ATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTGC	CGATAGCAAA	AAGAC	TTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAG	GGAGC	GGAAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACA	AGTAC	GATCCGGA	CTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCG	AAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAG	ATGCA	TGGCTCAAGA	GGTAG		2325

Deep Vent

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

ATGATACTTG	ACGCTGACTA	CATC	ACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTT	GAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATT	GATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCGGGG	180
AAGATAGTGA	GAATTATAGA	TGCC	GAAAAG	GTAAGGAAGA	AGTTCTTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAAC	ACCCCT	CAGGAC [XXX]	<u>NNNC</u>	CCGCAATAAG	GGATAAGATA 300
AGAGAGCATT	CCGCAGTTAT	TGAC	ATCTTT	GAGTACGACA	TTCCGTTCGC	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCA	ATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAA	GGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCC	AAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGG	GAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCT	ACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATA	AAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAG	CGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATA	AAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAG	AAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAGG	GACTGGAGAG	AGTT	GCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCA	ATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCA	ACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCT	CCAAAC	AAGCCGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGA	TACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCTAG	GAGC	CTGTAC	CCCTCGATAA	TAATCACCCA	TAACGCTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGG	TGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGG	TTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATG	AAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAA	ATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAG	GAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGA	ACTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACA	ATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATA	AAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCT	TTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGG	CTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTA	GAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACT	GAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACG	AGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCC	GCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGAC	GGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTAT	GACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ID NO: 40)

ATGATCCTTGACGTTGATTACATCACCAGAAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCAGTTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTACGCACCCGCAGGAC [XXX] NNNCCGGCAATCCGCGACAAAATAAGGAAGCACCC
CGCGGTTCATCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAA
GGTGAGGAAGAGCTTAAACTCATGTCTTCTGACATCGAGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGA
TTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCTTCTTTACGTTGAGGT
TGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAC
AACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACG
GGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCC
AGTCATAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAG
AAGGTCACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGG
ACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCT
CTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTCTAAGGAAGGCCTACGAGAGGAACGAACCTC
GCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgCGGTGGCTACGTCAAGGAGCCGGAGC
GGGGACTGTGGGACAATATCGTGTATCTAGACTTTCTAGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCC
AGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTGCGTCAAGTTCTGCAAGGACTTCCCC
GGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACC
CGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATC
AGAGAGCTTGAGGAAAAGTTTCGGTTTTTAAAGTCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTCGAGCGG
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAGTCCCCGGCCTTCTCGAACTCGA
ATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAAGTACGCGGTTCATCGACGAGGAGGGCAAGATAACC
ACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGAGGCGAGGGTTTTGGAGGCGATAC
TCAGGCACGGTGACGTTGAAGAGGCCGTGAGAATTGTGAGGGAAGTACCGAAAAGCTGAGCAAGTACGAGGTTCCGCC
GGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGCCCGCACGTAGCCATAGCG
AAgGTTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAAGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGA
TAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCACAGTACGATGCGGACTACTACATCGAGAACCA
GGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCGAG
GTCGGGCTTGCGCGCTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

MARKED UP VERSION OF AMENDED FIGURE 13B

Please replace Figure 13B with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13B.

Figure 13B

>Pfu V93R (SEQ_ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs //

>Pfu V93E (SEQ_ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/G387P (SEQ_ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TPGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKs

>Pfu V93R/D141A/E143A (SEQ_ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW

SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVGIVYIVLRGDGPISNRAILAEEDPKKKHYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>Pfu V93E/G387P (SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVGIVYIVLRGDGPISNRAILAEEDPKKKHYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>Pfu V93E/D141A/E143A (SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVGIVYIVLRGDGPISNRAILAEEDPKKKHYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKK

>DEEP VENT V93R (SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAOKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPYEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDIPGFIPSLLRLLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVGIVYIVLRGDGPISKRAILAEEDLKRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E (SEQ ID NO:48)

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAOKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPYEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDIPGFIPSLLRLLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVGIVYIVLRGDGPISKRAILAEEDLKRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R (SEQ ID NO:49)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDVVS TEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEYQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDVVS TEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEYQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R (SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVS TEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEITPAWETGENL
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLLDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E (SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVS TEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEITPAWETGENL
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFRFCKDFPGFIPSLLDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI

RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R (SEQ ID NO:53)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGGKTVRVLDVAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGLG
GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRLRT
TYLGGYVKEPEKGLWENIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSI LGDLIAM
RQDIKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGIFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLP AVALRILEAFGYRKEDLRYQSSQTGLDA
WLKR

>VENT V93E (SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGGKTVRVLDVAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGLG
GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRLRT
TYLGGYVKEPEKGLWENIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSI LGDLIAM
RQDIKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGIFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLP AVALRILEAFGYRKEDLRYQSSQTGLDA
WLKR

>JDF-3 V93R (SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSSTEKEMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLPYVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEIEATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCDFPGFIPSL LGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVVEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E (SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSSTEKEMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLPYVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEIEATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCDFPGFIPSL LGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVVEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

MARKED UP VERSION OF AMENDED FIGURE 14

Please replace Figure 14 with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 14.

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

```
5'
atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc      48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile

1           5           10           15

agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga      96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg

          20           25           30

aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att      144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile

          35           40           45

gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg      192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg

          50           55           60

gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata      240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile

65           70           75           80
```

Marked-Up Version

gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc 288

Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile

85

90

95

agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac 336

Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr

100

105

110

gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg 384

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro

115

120

125

atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg 432

Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr

130

135

140

ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata 480

Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile

145

150

155

160

agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc 528

Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile

165

170

175

gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag 576

Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys

180

185

190

Marked-Up Version

cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc	624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	

195	200	205
-----	-----	-----

tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	

210	215	220
-----	-----	-----

aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	

225	230	235	240
-----	-----	-----	-----

atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	

245	250	255
-----	-----	-----

cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	

260	265	270
-----	-----	-----

tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	

275	280	285
-----	-----	-----

aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	

290	295	300
-----	-----	-----

tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat	960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr	
305	310
	315
	320

gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc 1008
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335

gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc 1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca 1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac 1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr
370 375 380

gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc 1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
385 390 395 400

gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat 1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
405 410 415

Marked-Up Version

aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac	1296
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp	

420	425	430
-----	-----	-----

gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc	1344
Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe	

435	440	445
-----	-----	-----

atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag	1392
Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys	

450	455	460
-----	-----	-----

aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat	1440
Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp	

465	470	475	480
-----	-----	-----	-----

tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac	1488
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr	

485	490	495
-----	-----	-----

tac ggc tat gca aag gcc cgc tgg tac tgc aag gag tgc gcc gag agc	1536
Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser	

500	505	510
-----	-----	-----

gtt acc gct tgg ggc agg cag tac atc gag acc acg ata agg gaa ata	1584
Val Thr Ala Trp Gly Arg Gln Tyr Ile Glu Thr Thr Ile Arg Glu Ile	

515	520	525
-----	-----	-----

gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt 1632

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe

530

535

540

ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca 1680

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa 1728

Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu

565

570

575

ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag 1776

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt 1824

Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu

595

600

605

gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg 1872

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

agg gtt ctt gag gcg ata cta aag cac ggt gac gtt gaa gaa gcg gta 1920

Arg Val Leu Glu Ala Ile Leu Lys His Gly Asp Val Glu Glu Ala Val

625

630

635

640

Marked-Up Version

agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca 1968

Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645

650

655

ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac 2016

Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp

660

665

670

tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca 2064

Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala

675

680

685

agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc 2112

Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690

695

700

aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt 2160

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705

710

715

720

gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag 2208

Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln

725

730

735

gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa 2256

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

740

745

750

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg 2304

Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp

755

760

765

cta aaa cct aag aca tga 2322

Leu Lys Pro Lys Thr

Figure 17A

Pyrococcus furiosus gene for archaeal histone (Hmf-like) [Fig.17-A]

(ACCESSION No: AB013081)

Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 64)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA 207
```

Figure 17B

(Hmf-like)-Taq DNA polymerase fusion protein [Fig.17-B]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC
```

```

      G   G
    // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]V100 Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC100 TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

```

A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTC
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G GGC GGC GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 CTG GCC GGC AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R G Y

```

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
V   E T L F G R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

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Figure 17C

Taq DNA polymerase- (Hmf-like) fusion protein [Fig.17-C]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

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G   G   G
// GGC GGC GGT

```

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V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

```


D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]Y Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GAG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTG CTC GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTC GGC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E	
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG	
E M G A R M L L Q V H D E L V L E A	
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC	
P K E R A E A V A R L A K E V M E G	
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG	
V Y P L A V P L E V E V G I G E D W	
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG	
L S A K E G I D G R G G G H H H H	
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT	
H H //	
CAT CAT //	
M M G E L P I A P V D R L I R K A G	18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
A Q R V S E Q A A GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
K A I E I A K K A V D L A K H A G R	54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
K T V K V E D I K L A I K S *	
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA	69

Figure 17D

Pfu DNA Polymerase (WT) -(Hmf-like) fusion protein [Fig.17-D]

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

//
ccctggctct gggccacat atatgttctt actcgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataagtattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagAAC atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaaggcct
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tcacgaagga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca agggagaagt acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaatctt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagccctgg gaaagtggag agaacccttga
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tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgaa tatatgagca

gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
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aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
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ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgt ctcactcaag ccccatatgg gttgagaaaa

```

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttg //
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```

Figure 17F

(HMF-like) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-E]

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggctct ggggtccacat atatgttctt actcgccctt atgaagaatc ccccgatcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatagt tatagagaag
gtttttact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaaac atccagcagt

```


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tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaaccttga
gagagtgc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaagaat
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaag
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gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatatag gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
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gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
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ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttccccgacc caagtcgcgt

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acaatttttt ccttgatatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccggggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgctctctttt
taacttttac agaaataact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnmn mngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntcccnga
aagattgaga tgttcttgg // TGA

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Figure 17F

(Hmf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-F]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT      54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA      162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

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//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240

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ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGGCAG AAAAACCCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGAGAGGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAAG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACATAGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAGAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCTGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAAAC TC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGACAAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA

```

Figure 17C

PFU DNA POLYMERASE (V93 R OR E) - (HMf-like) fusion protein [Fig.17-G]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTATTATTAG GCTATTCAAA 60
AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA ATTACTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCAATCCC ATATTAGCG 660
AAAAGGCGAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACTTAT 960
GAACTCGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGTG GGAAGAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTTCC ACCAGAGAAG 1980

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CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGGATCCCA AAAAGACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) - (Hmf-like) fusion protein [Fig.17-H]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

**G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)**

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC TTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCAATTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TTCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020

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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
AAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

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//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17

(Hmf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein [Fig.17-I]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
 AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
 TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGATG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTATG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAGAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG TGCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGTTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAA TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTTCAC 2040
 GTAGCTGTTG CAAAGAAAAC AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100

GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGTACTTA GGATTTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17J

(HMF-LIKE) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein
[Fig.17-J]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840

GCAATTTTGT GAAAGCCAAA GGAGAAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACTTTGTAG AGTGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACA [CCN]GGT GGAATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCGGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATAGAT ATAAGGCAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17K

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein

[Fig.17-K]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATT CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCGAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACA [CC N] GGTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAAGCAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAAGTCCCTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160

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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Figure 17L

KOD DNA POLYMERASE - (Hmf-like) fusion protein [Fig.17-L]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63)

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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACATGACTA CATAACCGAG GATGGAAAGC CTGTACATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCG CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGCTCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CTTAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCAGAG GAGGGTTGTG GGAGAACATA 1200

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GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCG AGCTTGTCTG GAGACCTCTT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCTGTACG AAGAAGAAAT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGAGG CGAGGGTTCT TGAAGCTTTG CTAAGAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG GTC GCA ATT AAG AGC TGA

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Figure 17M

(Hmf-like) - KOD DNA POLYMERASE fusion protein [Fig.17-M]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

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//ATGATCTCTG ACACGTGACTA CATAACCGAG GATGGAAGC CTGTACATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCGGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTTCG CAAGCGCTAC 360
CTCATAGACA AGGATTTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCCTTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCTTAC 540
GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTACAGAGG TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGCTTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGGCGAG ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTACACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCAGAG GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CTTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGCGC CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGGCTT CTTCTGTACG AAGAAGAAGT ATCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCGAG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTAC AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17N

(Hmf-like)-vent DNA POLYMERASE FUSION PROTEIN [Fig.17-N]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
      GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
      AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
      AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
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ATGATACTGG ACACGTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCAIT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGTCTGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGTCAATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTGTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTAAAT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
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AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCAATAAA 1680
AAGAAAGCCA AGGAATTCCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AACAGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACATT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTGC CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGNATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17Q

Vent DNA POLYMERASE - (Hmf-like) FUSION PROTEIN [Fig.17-O]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG AACTGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGA GAGTCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCCTTTC CAAGCGTTAT 360
CTCATATGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAACACG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960


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ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAACCTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTTATTTTGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTTATTCCTT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACA TTAGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA AGTTCGGCTT TAAGGTTCTT 1620
TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTCCACATT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATA GCGATAGGTT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```

Figure 17P

Deep Vent- (Hmf-like) DNA polymerase fusion protein [Fig.17-P]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120

CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGGG GAGGCCGATT 240
 GAGGTATGGA GGTGTACTTT TGAACACCTT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
 AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAGAGAGTAC 360
 CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT 420
 GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGGTAG TTTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
 AAAGATCCCG ATGTTATAT TACCTACAAC GCGGATCTTT TCGACCTTCC CTATCTAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAAG 720
 ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
 TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
 GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGGAG 900
 ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCATGG AGGATGCAA GGTAAACGTAC 960
 GAGTCGGTA GGGAGTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
 CTGTGGGATG TTTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
 GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
 CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
 TTAGTTTCCC TAGATTTTCA GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320
 AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
 AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
 GATTACAGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
 GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
 TATATAGAT TCGTAAGGAA GGAACCTGGAG GAAAAGTTTCG GGTTCAAAAGT CTTATACATA 1620
 GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
 GCCCTAGAT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
 GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
 GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
 AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
 GTAAAGATAG TTAAGGAGGT AACTGAAAAAG CTGAGCAAAGT ACGAAATACC TCCAGAAAAAG 1980
 CTAGTTATTT ACGAGCAGAT CACGAGGCCCT CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
 GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
 GGGTACATAG TTTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
 TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
 GCCGTTCTTA GAATATTAGA GGCTTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
 ACTAAACAGA CAGGTCTTAC GGCAATGGCTT AACATCAAGA AGAAG // 2328

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17Q

(Hmf1like) - Deep Vent DNA polymerase fusion protein [Fig.17-Q]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CAITTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCGC GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGAG GACTGGAGAG AGTTGCAAAG TATTTCAATGG AGGATGCAAA GGTAACGTAC 960
GAGTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTICAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320

AAGTTCTGCA	AGGACTTCCC	GGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTCTG	GGTTCAAAGT	CTTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GC'TTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACGTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCAACGAGT	ACAAGGCTAT	AGTCCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGTTGATA	2100
GGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (Hmf-like) fusion protein [Fig.17-R]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTTCAGGATTGAATACGACCGCGAGTTTCGAGCCCTACTTCT
ACGGCTCTCAGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCGCGGGAGAAAGGTGAAGAAAAAGTTTCTCTCGG
CAGGTCGTGGAGGTCGTGGTCTCTACTTTCACGCACCCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTTCATCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGGAGATGAGACGCTCTACCAAGGAGGAGAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATTAACCTGGAGAAGATCGACCTTCTTACGTTGAGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGGGGTCTTAAGGAGAGGACCCGGACGTGTGATAACATACACGGCGACAACTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTCGGAGGAGCGGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGAGACCCGGCGAGGGCTTGAGAG
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGTACCGCTGGAGACCCGGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGCTCCAGCACCCGGCAACCTCGTCGAGTGGTTCTCTCTAAGGAAGCCCTACGAGAGGAACGAACTCGTCCCAACAAAGCCCGACGAGGAGGAGTGGCGAGGAAGGGGGGCT
ACgcCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATAAATCACCCACAAACGTCTCGCCAGATAC
GCTCAACCGGAGGGGTGAGGAGCTACGACGTTGCCCCCGAGGTCCGTCAAGTTCTGCAAGGACTTCCCGGCTTCAATTCGAGCCTGTCTCGGAAA CCTGTGGAGGAAAGG

CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCCGCTGGAGAAGAATCTCTCGAATTACAGGCAACGCGCATCAAGATTCTCGCCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGTTACTGACGGAGTGC CGCAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTTCGGTTTTTAAAGTCTCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATCTCTGGAGCGGACGCTGAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCGTACGAAGAAAAAGTACCGGTCTATCGACGAGGAGGCAAGATAACCAACGCGCGGCTTGAGATAGTACAGCGCG
ACTGGAGCGAGATAGCAAGGAGACGCGAGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGAAGAGCGCTCAGAAATTGTCAAGGAAGTCAACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAACTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAAGcGTTTGGCCCGCCAGAGGT
GTTAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCAACAAGTACGATG
CGGACTACTACATCGAAGAACGAGTTCTGCGGCGAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTCGGCTACCAAGAAGACGAGGCGAGTCTGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGAAGAAG//

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17S

(Hmf-like) - JDF-3 fusion protein [Fig.17-S]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCTATCAGGGTCTTCAAGAAGGAGAACCGCGAGTTCAAGATTGAATACGACCGCGAGTTCGAG
CCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCCATCGAAGAAAATCAAAAAGATAACCGCGGAGAGGCACCGCAGGGTCGTTAAGTTTAAGCGCGGAGAAAGGT
GAAGAAAAAGTTCTCGGACAGGTCTGTGAGGTCTGGTCTCTTACTTCACGCAACCGCAGGACXXXCGGCAATCCGCGCAAAAATAAGGAAGCACCCCGCGGTCA
TCGACATCTACGAGTACGACATACCTTCGCCAAGCGTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGAGATC
GAGACGCTCTACCAAGGAGGAGAAGAGTTTGGAAACCGGCCGATTTCTGATGATAAGCTACGCCGATGAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCT
TCTTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAAGCGCTTCTTGAGGGTCGTTAAGAGGAAGGACCCGGAAGTGTGATAACATAACAACGGCGCAACT
TCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAGCTTGGCGTGAAGCTTTTACCTCGGAGGGAAGGAGCGGAGATACAGCGCATGGGGGACAGGTTTGGC
GTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTATAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAA
GCCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGCTTGAGAGGGTCTCGGCGCTACTCGATGGAGGACGCGGAGGGTTTACCTACG

AGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCCGCTCCAGCACCCGGCAACCTCGTCGAGTGGTTCC
CTCCTAAGGAAGGCCCTACGAGAGGAAACGAACTCGCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAAGGGGGGCTACgCCGGTGGCTACGTCAAGGAGCC
GGAGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTTCGTAGTCTCTACCCCTTCAATCAATAATCAACCAACAGTCTCGCCAGATACGCTCAAACCGCGAGGGGT
GTAGGAGCTACGACGTTTGCCCGGAGGTCGGTCAAAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAAGATA
AAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGAAATCTCTCGATTACAGGCAACGGCCATCAAGATTCTCGCCAAACAGCTACTACGGCTACTACGGCTA
TGCCAGGGCAAGATGGTACTTGCAAGGAGTGGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAGTTTGGGAAAGTTCCGGTTTTA
AAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTTAAACTATATCAATCCCAAA
CTGCCCCGGCTTCTCGAACTCGAATAACGAGGGCTTCTACGTACGGGGCTTCTTCGTCAAGAAAGTAACGGGTCTATCGACGAGGGGCAAGATAACCCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGACGCGAGGGTTTGGAGGCGGATACTCAGGCACGGTGACGTTGAAGAGGCCCGTCAGAA
TTGTCAAGGAAGTCAACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTCAAGGCCACCCGGC
CCGCACGTAGCCATAGCGAAGCGTTTGGCCCGCAGAGGTGTAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAG
GGCGATTCCCCTTCGACGAGTTTCGACCCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGAGAAACCAAGTTCTGCCCGCAGTTGAGAGAAATCCTCAGGGCCCTTCG
GCTACCCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTTCGGGCTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archaeal histone (HMF-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082) [Fig.17-T]
/product="pcna sliding clamp (proliferating-cell nuclear antigen) "

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486

E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			750

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein [Fig.17-U]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90

ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 L K K G E E N F L E I T I Q G T A T 108
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 R T F R V P L I D V E E M E V D L P 126
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 E L P F T A K V V V L G E V L K D A 144
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 V K D A S L V S D S I K F I A R E N 162
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 E F I M K A E G E T Q E V E I K L T 180
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 L E D E G L L D I E V Q E E T K S A 198
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 Y G V S Y L S D M V K G L G K A D E 216
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 V T I K F G N E M P M Q M E Y Y I R 234
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 D E G R L T F L L A P R V E E 250
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG

G G G
 // GGC GGC GGT

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
 D G H H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A L K E D G D A V I V V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

 S F R H E A Y G G Y K A G R A P T P
 TTC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CGG GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC CGC CTA GAG GCC CGG GTG
K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
L S A K E G I D G R G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

Figure 17V

Taq DNA polymerase-(PCNA) fusion protein [Fig.17-V]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

```

      G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]Y   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
```

GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CCG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC GTG CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTG GAG GCC
L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT
S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG

 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

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L S A K E G I D G R G G G G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT

H H //
CAT CAT //

M P F E I V F E G A K E F A Q L I D 18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54

T A S K L I D E A A F K V T E D G I 36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108

S M R A M D P S R V V L I D L N L P 54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162

S S I F S K Y E V V E P E T I G V N 72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216

M D H L K K I L K R G K A K D T L I 90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270

L K K G E E N F L E I T I Q G T A T 108
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324

R T F R V P L I D V E E M E V D L P 126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378

E L P F T A K V V V L G E V L K D A 144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432

V K D A S L V S D S I K F I A R E N 162
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486

E F I M K A E G E T Q E V E I K L T 180
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540

L E D E G L L D I E V Q E E T K S A 198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594

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Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216	
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648	
V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234	
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250	
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA				

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein [Fig.17-W]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

//
ccctggtcct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gtttttact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagttct cggcaagcct attaccgtgt ggaaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaaag
gtcaagcaca gggaaccttg tagagtgggtt cttacttagg aaagcctacg aaagaaaacga
agtagctcca acaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtaggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
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ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggattttaa agtcctctac attgacactg atggctctcta
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tcgtgggtta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agtttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaaga
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aggcgatggg ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
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aagattgaga tgttcttgg //
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ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG
TCA AGC ATA TTT AGC AAA TAT GAA GGT GTT GAA CCA GAA ACA ATT GGA GTT AAC
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA
AGA CCA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA
GAA CTT CCA TTT ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA
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108
162
216
270
324
378
432
486
540
594
648
702

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GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-X]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
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AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG
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agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
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caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggaggggttt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
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ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-Y]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGGA AAAACATAGA TCCTCCATAC 540
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 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
 TATCATGTAA TACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
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 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTACGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA 1080
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 CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
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 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAAACTCTTA GCTGAGAGCG TTACTGCCCTG GGAAGAGAA 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAGAA 1560
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 GAAGGGTTTT ATAAGAGGGG ATCTTCTGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
 // TGA

Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) -(PCNA) fusion protein [Fig.17-Z]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTTAG ATGTGGATTAA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCITCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTTATAAT GGAGACTCAT TCGCAITCCC ATATTTAGCG 660
AAAAGGCGAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
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CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAITCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAGAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCITGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800

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GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
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AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA AAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

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Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E) -(PCNA) fusion protein [Fig.17-AA]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACCTT TTAGACCATA CATTTACGCT 120

CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITTGCCCTTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACTTTGTAG AACCTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AGCCAAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTGG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCGGATACCT TAAATCTTGA GGGATGCAAG AACATATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGGAAAGAAA 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAAGAAGT AATACAAAAAG CTTTGCCAAIT ATGAAATTC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGCCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAGAAACT AGCTGCTAAA GAGTTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC // 2328

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// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GAA GTT GAA GAG TGA

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Figure 17BB

(PCNA) - pfu DNA POLYMERASE (G387P/V93R OR E) fusion protein [Fig.17-BB]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

**G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)**

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432

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GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAAGGAAAAA CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCCTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAAGG 1140
 CTCAGGGAGA GCTACACACC NGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTTCGATTA TAAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAATAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860

AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TAGCATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17CC

(PCNA) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein [Fig.17-CC]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GGT GAA GAG //	

//ATGATTTTAG ATGTGGATTATA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGGTG ATTACTTTGA AAAACATAGA TCttccATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTTATGGGATG TTTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA [CC N] GTT GGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACATATCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGCGGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCttCCA 2220

GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17DD

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (PCNA) fusion protein
 [Fig.17-DD]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
 GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTTCTT ACTTAGGAAA 1080

GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACA[CC N]GTT GGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
 ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
 AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
 TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
 ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17E

KOD DNA POLYMERASE - (PCNA) fusion protein [Fig.17-EE]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG AACTGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGAATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGG GAGTTGCGG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACCTGGA TCTCCCCTAC 540
GTTGACGTGC TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATAACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGTTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCCTGGGA 900
ACCGGCGAGA ACCTTGAGG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCAATAC 960
GAGCTTGGGA AGGATTCTCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCAGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCTGGCA AACAGTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CCGCCTGGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620

ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680	
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGCG	CGCTTGAGCT	CGAGTACGAG	1740	
GGCTTCTACA	AACGCGGCTT	CTTCGTACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800	
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860	
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920	
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980	
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCCG	TCCCCACGTT	2040	
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100	
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GCGACACAGG	CGATACCGTT	CGACGAGTTC	2160	
GACCCGACGA	AGCACAAATA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCAGCC	2220	
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280	
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CT	2325		
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC CAA CTT ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAT	GAG GCC	GCG TTT	AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GTT	GTC GTG	ATT GAC CTA AAT CTC CCG	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAA	CCA CCA	GAA ACA ATT GGA GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG GAC ACC TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC AAC	TTC TTA	GAG ATA	ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA GTT GAC CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	GTA GTT	GGA GTC CTA AAA GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT GCC AGG GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	ACC CAG	GAA GTT	GAG ATA AAG CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG ACA AAG AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GTT	AAA GGA	CTT GGA AAG GCC GAT GAA	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG TAT TAC ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA GAG TGA	

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein [Fig.17-FF]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATGACA AGGGATTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTGCGCG AGGGGCCAAT CCTTATGATA 480
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GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
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TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTTCT TCCGATGGAG GCCCAGCTTT CTGCTTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTTCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
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ACCGACGGAT TTTTGTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
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GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCGAG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
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GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGTTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTC TCAAGGGCTC TGGGAGGATA GGCACACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17GG

(PCNA) -vent DNA POLYMERASE FUSION PROTEIN [Fig.17-GG]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAATT TTGATTTGCC GTATCTCATA 660
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CCCAAGATTG AGAGGATGGG TGATAGTTTT GTGTGGAAA TCAAGGGTAG AATCCACTTT 780
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TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
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ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
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GCAATGAGC AAGATATAAA GAAGAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
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TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
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GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAAGGAGAG TTTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG TAG 2325

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN [Fig.17-HH]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGTCTGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCGTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCATATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGTCAT ACGCAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CTGGGAGGA TATGTAAAG AGCCAGAAA AGTTTGTGG 1200
GAAAATATCA TTTATTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAC 1260
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GGATATAGT TCTGCAAGGA CTTTCCGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACA TTAGACCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTCTG AAAAGCGTTAC CGCATGGGG 1560
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TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTA	1680
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GAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGG	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAATAG	CAAAATACAG	GGTTCACATT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTGG	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAAGGGAGC	GGAAAGATAA	GCATAGGGT	AAATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GG 2325	//	

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein [Fig.17-II]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACCTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	CGGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
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GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
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GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAAGT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAAG	GACTGGAGAG	AGTTGCAAAG	TATTCATGGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500

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GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
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GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGTGTTTGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTTCGT ACGAAGAAGA AGTATGCCGT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGCTTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAT CCA AGT AGA GGT TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GGT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GGT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT CAA GAG GAG ACA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

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Figure 17.II

(PCNA) - Deep Vent DNA polymerase fusion protein [Fig.17-JJ]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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//ATGATACTTG ACGCTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCTT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
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AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAAGAGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGCCAAA	GGAGAAAGTT	TACGCTCAG	AGATAGCTGA	GGCCTGGGAG	900
ACTGAAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCTG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATT	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCAC'TAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAAACC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AAC'TGAAAAG	CTGAGCAAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCAAGAGT	ACAAGGCTAT	AGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTT'TACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17KK

JDF-3 - (PCNA) fusion protein [Fig.17-KK]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCCGTCAATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGAGGACGGCAGGTCGTTAAGTTAAGCGCGGAGAGAGTGAAGAAAAGTTCTCTCGG
CAGGTCGTGGAGGTCGTGGTCTCTACTTACGCACCCCGAGGACXXXCCGGCAATCCGGACAAATAGGAAGCACCCCGCGGTTCATCGACATCTACGAGTACGACATACCC
TTCCCAAGCGCTACCTCATAGACAAGGCTTAATCCCGATGGAAGGTGAGGAAGCTTAAACTCATGTCTTGGAGTGGAGAGAGTGGAA
CCGGCCGATTCGTATGATAAGCTACGCCGATGAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGGGGTCTTAAAGGAAGGACCCGACGTGTGATAACATACAAACGGCGACAACTTCGACTTCGCCCTACCTCGACCTTTATCCAGTCAATAAGCGCACCATAA
ACCTCCGGAGGACGGGACGCGCAAGATACAGCGCATGGGGACAGGTTTGGCGTCGAGTGAAGGACGGGTACACTTCGACCTTTATCCAGTCAATAAGCGCACCATAA
ACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGACGCGAGGTTACCTACGAGCTTGGCAGGAGTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCTAAGGAAGGCTTACGAGAGGAACGAACTCGCTCCCAACAAAGCCCGACGAGAGGAGCTGGCGAGGAAGGGGGGCT
ACGCCGTGGCTACGTCGAAGGAGCCGGAGCGGGGACTGTGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCATAAATCACCCACAACGTCCTCGCAGATAC
GCTCAACCCGAGGGGTGTAGGAGCTACGAGCTACGACGTTGCCCGGAGGTCGGTCAAAAGTTCTGCAAGGACTTCCCGGCTTCAATCCGAGCTGTCTCGGAAACCTGTGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCTCGATTACAGGCAACGCGCTATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGTTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAACTCGAATACAGAGGCTTCTACGTACAGGGCTTCTTCTGTCACGAAGAAAAAGTACCGCGTCAATCGACGAGGAGGCAAGATAACACCGCGGGCTTGAGATAGTCAGGCGG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGCGAGGGTTTGGAGGCGATATCTCAGGACCGGTGACGTTGAAGAGGCCGTAGAAATTTGTACAGGAAGTCAACGAAAAAGTGAACAA
GTACGAGGTTCCGCGGAGAACTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTCAAGGCCACCGGCCCGCAGTAGCCATAGCGAAGcGTTTGGCCCGCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCAACAAGTACGATG
CGGACTACTACATCGAAGAACCAAGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCTTCCGCTACCGCAAGGAAGACCTGGCTACCAGAAGACGAGGCGAGTTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54

ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC		216
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT		540
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	ACA	AAG	AGC	GCA		594
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17LL

(PCNA) - JDF-3 fusion protein [Fig.17-LL]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC		216
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
GAA	TTT	ATA	ATG	AAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	GAG	ATA	AAG	CTA	ACT		540
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594

TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	CAA	ATG	GAG	TAT	TAC	702
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	//			

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTTCATCAGGGTCTTCAAGAAAGGAGAAACGGCGAGTTTCAGGATTGAATACGACCCGCGAGTTTCGAG
 CCCTACTTCTACGCGTCTCTCAGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGGAGAGGCACGGCAGGGTCGTTAAAGTTAAAGCGCGGAGAAAGGT
 GAAGAAAAAGTTCTCGGCAGGTCGTGGAGGTCGTGGTCTCTACTTTCACGCACCCCGCAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTCA
 TCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCTTQGAQATC
 GAGACGCTCTACCCAGGGGAGAAGAGTTTGGAAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCT
 TCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAAGCGTCTTTGAGGGTCGTTAAGGAGAAGGACCCCGACGTCGTGATAACATACAACGGCGACAACCT
 TCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTTACCCCTCGGAGGACCGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGG
 GTCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAA
 GCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTTGGAGACCGGCGAGGGCTTGAGAGGTCGCGCGTACTCGATGGAGGACGCGAGGTTTACTTACG
 AGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCACGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC
 CTCTTAAGGAAGGCCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGGCTACGCGGTGGCTACGTCGAAGGAGCC
 GGAGCGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTCTAQCCTTCAATCAATAATCAACCAACGTCGCCAGATACGCTCAACCGCGAGGGGT
 GTAGGAGCTACGACGTTGCCCGAGGTCGGTCAAAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGTCGGAAACCTGCTGGAGGAAAGGCAGAGAATA
 AAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCTCGATTACAGGCAACGGGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA
 TGCCAGGGCAAGATGGTACTGCAAGGAGTGCCTGAGAGCGGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAAGGAAAAGTTCCGTTTAA
 AAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCAACGCG
 CTGCCCGGCTTCTCGAACTCGAATAACGAGGGCTTCTACGTCAGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCAACGCG
 CCGGCTTGAGATAGTCAGGCGGACTGGAGCGGATAGCGAAGGAGACGCGAGGAGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCGGTCAGAA
 TTGTCAAGGAAGTCAACGAAAGCTGAGCAAGTACGAGTTCCGCCGGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTCAAGGCGCCACCGGC
 CCGCACGTAGCCATAGCGAAGCGTTTGGCCCGCAGAGGTGTTAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAG
 GCGGATTCCTTCGACGAGTTCGACCCGACGAAGCAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGCGAGTTGAGAGAAATCCTCAGGGCCTTCCG
 GCTACCGCAAGGAAGACCTGCGCTACCCAGAAGACGAGGCGAGTTCGGGCTTGGCGCGTGGCTGA

Figure 17MM

Sac7d gene (ACCESSION No: M87569) [Fig.17-MM]

Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 70)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S	18
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GTA	GAC	ACT	TCA	54
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D	36
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC	108
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L	54
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA	162
L	D	M	L	A	R	A	E	R	E	K	K	*						67
TTA	GAC	ATG	TTA	GCA	AGA	GCA	GAA	AGA	GAG	AAG	AAA	TAA						201

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein [Fig.17-NN]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

M	V	K	V	K	F	K	Y	K	G	E	E	K	E	V	D	T	S
ATG	GTG	AAG	GTA	AAG	TTC	AAG	TAT	AAG	GGT	GAA	GAG	AAA	GAA	GTA	GAC	ACT	TCA
K	I	K	K	V	W	R	V	G	K	M	V	S	F	T	Y	D	D
AAG	ATA	AAG	AAG	GTT	TGG	AGA	GTA	GGC	AAA	ATG	GTG	TCC	TTT	ACC	TAT	GAC	GAC
N	G	K	T	G	R	G	A	V	S	E	K	D	A	P	K	E	L
AAT	GGT	AAG	ACA	GGT	AGA	GGA	GCT	GTA	AGC	GAG	AAA	GAT	GCT	CCA	AAA	GAA	TTA

```

L D M L A R A E R E K K //
TTA GAC ATG TTA GCA AGA GAA GAG AAG AAA //

  G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K

```

GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E E R L L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GCC GTC CTG GAG GCC
 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC
 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG
 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT
 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG
 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GGC GTG GAC CCC CTG ATG CGC CGG GGC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
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 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG

 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

 L S A K E G I D G R G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT

 H H *
 CAT CAT TAA

Figure 1700

Taq DNA polymerase-Sac7d fusion protein [Fig.17-00]

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

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      // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   [X]Y   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGC GGC GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
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D L Y Q L L S D R I H V L H P E G Y
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L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CCG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG GGC GGC GTG CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

G E W T E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A N L W G R L E G E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A A F I A E E G W L L V A L D Y

ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAG GTG CTC GTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

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L S A K E G I D G R G G G G G H H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGG CAT CAT CAT CAT

H H //
CAT CAT //

M V K V K F K Y K G E E K E V D T S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

K I K K V W R V G K M V S F T Y D D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N G K T G R G A V S E K D A P K E L-
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

L D M L A R A E R E K K // *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

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Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein [Fig.17-PP]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)

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caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

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aagattgaga tgttcttgg //

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AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

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TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein [Fig.17-QQ]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

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AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
//
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tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
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tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cagtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttccccacc caagtccgct
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtcctctc
ctcgatttcc ttggttgtagc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-RR]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
 //ATGATTTTATG ATGTGGATTAT CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACCTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTATTCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
 TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGTCCCAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTATG AGCCCTATAT CCTTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAA TTAAGACAAA AATGNAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAGGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG TGTCTATATG AACTATCCCA AAGAGGAGAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGTTTTT ATAAGAGGGG ATTCTTCTGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTATAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAAG CTTTGCCAATT ATGAAATTC ACCAGAGAAG 1980

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CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGAT AGTCTCTAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA

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Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein [Fig. 17-SS]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTTAATG GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACT 1020

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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

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Figure 17T

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein [Fig.17-TT]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTTGA AAAACATAGA TCITCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCAITCCC ATATTTAGCG 660
AAAAGGCGAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCTTCGATTA TAAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACCTCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTCAC 2040

GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein [Fig.17-UU]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCACAGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCCTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCTTC 420

GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAANAATGA AGCAAAAGGTG ATTACTTTGGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGTTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGAGA GCTACACA [CC N] GTTGGATTCTGTT AAAGGCCAG AAAAGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACATATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

Figure 17VV

SAC7D-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein [Fig.17-VV]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
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//ATGATTTTATG ATGTGGATTATA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAAGCTT TTAGACCATATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCTTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITGGCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TCITCCATAC 540
GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACCTGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGATG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
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CTCAGGAG GCTACACA [CC N] GTTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
 AAGTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGC AAAAGCGAT AAAACTCTTA GCAAATTCCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAAITCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCTGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGCGGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein [Fig.17-WW]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATCTCG ACATGACTA CATAACCGAG GATGGAAAGC CTGTCAATAAG AATTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTTCAAGAAGA TAACGCCCGA GAGGCACGGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAAG GTTCAGAGA AGTTCTCGG GAGACCAGTT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTTCG 360 CAAGCGCTAC 360
 CTCATAGACA AGGGAJTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420 GCTCGCCTTC 420
 GACATTGAAA CTCCTTACCA TGAGGGCGAG GAGTTTCGCG AGGGCCCAAT CTTTATGATA 480 CTTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGG AGAACGTGGA TCTCCCTTAC 540 TCTCCCTTAC 540
 GTTGACGTG TCTCGACGGA GAGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600 TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660 CTATCTGAAA 660
 AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720 CGAGCCGAAG 720
 ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTTCGATCTC 780 CTTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840 CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900 AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960 GGTCACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020 CGGCCAGTCC 1020
 CTCCTGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CTTCAGGAAG 1080 CTTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCGGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140 GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200 GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260 CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320 CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380 AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440 GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGTACT ACGTTTACTA CGGCTATGCA 1500 CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560 AAGGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620 CTACAGCGAC 1620
 ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680 AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740 CGAGTACGAG 1740
 GGCTTCTACA AACGGGCTT CTTCTGCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800 AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860 GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920 GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980 GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040 TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAAATAC GCCCTGGAAC GGTGATAAGC 2100 GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCAGACGGG CGATACCGTT CGACGAGTTC 2160 CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220 TCTCCAGCC 2220
 TTGTAGAGAA TTCTGAGAGC CTTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280 CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
 // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA AAG AAG AAA // TGA

Figure 17XX

Sac7d - KOD DNA POLYMERASE fusion protein [Fig.17-XX]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //
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//ATGATCTCTG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTTAC 540
GTTGACGTCTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCCTGGGAA 900
ACCGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATCGGAA GGTCACTAC 960
GAGCTTGGGA AGGAGTCTCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
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GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCCTGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCTGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGCA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGTTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGCACAGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17YX

Sac7d-vent DNA POLYMERASE FUSION PROTEIN [Fig.17-YY]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

ATGATACTGG ACACGTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT 120

CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCCAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGTCTATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCCTTTC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCTTT 420
 GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AAGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAATATCA TTTTATTTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAAGAAJTT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCTT CCATACTCGG GGACTTAAAT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATCGGGACA CTGACGGCTT TTAATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAAGGAGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAAA AAGACTTGGC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
 ATTAATAAGCT ATATCGTTCT CAAAGGGAGC GAAAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN [Fig.17-ZZ]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGTCAATTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG ACGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGTAT GGGAGCTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAA AGGTTTGTGG 1200
GAAATATCA TTTTATTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA 1260

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GTATCCCCAG ATACCCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAAAT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCCGAT CGAAAAAGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGCTT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein [Fig.17-AAA]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	CGGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTTCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGGCCAAA	GGAGAAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGAAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGTTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAAGTTCCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCAG	GGCTGTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCCGT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAAACC	AAGCAAAAAGT	CCTAGAGGCT	ATCTTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100

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GGGTACATAG TGCTGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

```

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein [Fig.17-BBB]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

```

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//ATGATACTTG ACCTGACTA CATCACCAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCATAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATT 420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTGAGGAGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600

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AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGCCG	AAAAGTCTCG	GATAAAGCTA	CCCCTGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGCCAAA	GGAGAAAGTT	TACGCTCAG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAACACAGT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTGTGTACTG	TAAAGGAGTG	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTCGCCGTG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17CCC

JDF-3 - Sac7d fusion protein [Fig.17-CCC]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGAGCTTATTACATCACCGAGAAATGGAAGAGCCCGTCTATCAGGGTCTTCAAGAAAGGAGAAACGGCGAGTTTCAAGATTAATACGACCGCGAGTTTCGAGCCCTACTTCT
ACGGCTCCTCAGGAGCGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCGCGGAGAAAGTTGAAGAAAAAGTTCCCTCGG
CAGGTCTGTGGAGGTCTGGTCTCTACTTCACGCACCCCGCAGGACXXXCCCGCAATCCGCGACAAAATAAGGAAGCACCCCGCGTTCATCGACATCTACGAGTACGACATACCC
TTCCCAAGCGCTACCTCATAGACAAAGGCTTAATCCCGATGGAAGGTGAGGAAGCTTAAACTCATGTCTTTCGAGATCGAGACCGCTTACCACGAGGAGAAAGAGTTTGGA
CCGGCCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GGCTTCTTTGAGGGTCGTTAAGGAGAAGGACCCCGACGTCTGATAACATACAAACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTCCGGAGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCCGAGGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTTCATAAGCGCGACCATAA
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGATAGCCACCGCTGGGAGACC GGCGAGGGCTTGAGAG
GGTCGCGCTACTTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGTCCAGCACCGGCAACCTCTGTCGATGTGTTCTCTTAAGGAAGCTTACGAGAGGAACGAACCTCGTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGGCT
ACgcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTTCGTAGTCTCTACCCCTTCAATCATATCAACCAACGCTCTCGCCAGATAC
GCTCAACCCGCGAGGGTGTAGGAGCTACGACGTTTCCCCCGAGGTCGGTCAAAAGTCTTGCAAGGACTTCCCCGGCTTCATTCGAGCCCTGCTCGGAAACCTGTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGAAATCTCCTCGATTACAGGCAACGGCGCTATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGCAAGATGTGTACTGCAGGGAGTGGCCGAGAGCGTTTACCGCATGGGAAAGGAGTACATCGAAATGGTTCATCAGAGCTTGAGGAAAGTTTCGGTTTAAAGTCTCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAACTCGAATACGAGGGCTTCTACGTACGGGGCTTCTTCGTCAAGAAAGTACTCAGGCACCGTGAAGGCGCTCAGAAATTTGTCAAGGAAAGTCAACCGCGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTGGAGCGGATACTCAGGCACCGTGAAGGCGCTGAGAAATTTGTCAAGGAAAGTCAACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGCAGTAGCCATAGCGAAGcGTTTGGCCCGCAGAGGT
GTTAAAATCCGGCCCGGAACGTGTATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCACAAGTACGATG
CGGACTACTACATCGAGAACCAGGTTCTGCGCGCAGTTGAGAGAATCTCAGGGCTTCGGCTACCGAAGGACGAGGACGAGGTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAG//

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein [Fig.17-DDD]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

// ATGATCCTTGACGTTGATTACATACCGAGAAATGGAAGCCGTCATCAGGTCCTTCAAGAAGGAGAACGGCGAGTTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTT
CTACGGCTCTCAGGACGACTCTGCCATCGAAGAAATCAAAGATATACCGGAGAGGCACGGCAGGTCGTTAAGTTAAGCGCGGAGAAAGGTGAAGAAAAAGTTTCCTC
GGAGGCTGTGGAGTCTGGTCTCTACTTTCACGCCACCGCAGGACXXXCCGGCAATCCGCACAAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATAC
CCTTCGCCAAGCGTACCTCATAGACAAGGCCCTAATCCCGATGGAAGGTGAGGAAGCTTAAACTCATGTCTTCTGAGATGAGAGAGTGG
AACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGGCGCGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATT
AAGCGTTCTTGAGGTCGTTAAGGAGAAGGACCCGACGTCGTGATAACATACACGGCGACAACCTTCGACTTCGCCTACCTGAAAAGCGCTGTGAGAAGCTTGGCGTGAGCT
TTACCTCCGGAGGACGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGGTGAGGTGAAGGCAGGTACACTTCGACCTTTATCCAGTCTAAGCGCACCAT
AAACCTCCGACCTACACCTTGAGCTGTATACGAGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAG
AGGTCGCGGCTACTCGATGAGGACGCGAGGTTACCTACGAGCTTGGCAGGAGTTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGACGTTT
CCCGCTCCAGCACCGGCAACCTCGTCGAGTGTCTCTTAAGGAAGGCTACGAGAGGAACGAACTCGCTCCCAAGCCCGAGAGGAGCTGGCGAGGAGAAAGGGGG
CTACgCCGGTGCTACGTCAAGGAGCCGAGCGGGGACTGTGGACAAATATCGTGTATCTAGACTTTTCGTAGTCTCTACCTTCAATCAATAATCAACCAACGTCTCGCCAGAT
ACGTCACCCGAGGGGTGAGGACTACGACGTTGCCCGGAGGTCCGTCACAAAGTTCTGCAAGGACTTCCCGGCTTCAITCCGAGCTGTCTCGGAAACCTGTGGAGGAAA
GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCTCGATTACAGGCAACGGCAITCAAGATTCTCGCCAAACAGCTACTACGGCTACTACGG
CTATGCCAGGCAAGATGGTACTGCAAGGAGTGCGCCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTC
CTCTATGCAGACACAGCGGTCTCCATGCCACCAATCTCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGCAATGGAGTTCTTTAACTATATCAATCCCAAACCTGCCCGGCTTC
TCGAATCTGAAATACGAGGCTTCTACGTACGAGGCTTCTTCGTACGAAGAAAAAGTACCGGTCTACGACGAGGAGGCAAGATAACCAACGCGGGGCTTTGAGATAGTCAGGCG
CGACTGGAGCGAGATAGCGAAGGAGACGCAAGCGAGGGTTTTGGAGGCGATACTCAGGCAACGTTGAAAGAGGCCGTCAAGATTGTCTAGGGAAGTCAACGAAAAAGCTGAGC
AAGTACGAGGTTCCGCCGGAGAAAGCTGTGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTCAAGGCCACCGGCCCGCAGTAGCCATAGCGAAGcGTTTGGCCCGCAGAG
GTGTTAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCAAGTACGA

TGCGGACTACTACATCGAGAACCCAGGTTCTGCCGGCAGTTTGAGAGAAATCCTCAGGGCCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAAGAACGAGGCAGGTCGGGCTTGGC
GCGTGGCTGAAGCCGAAGGGGAAGAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene [Fig.17-EEE]:

Nucleotide sequence (SEQ ID NO: 71)

Amino acid sequence (SEQ ID NO: 72)

```
A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein [Fig.17-FFF]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
// A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K  //  G  G  G
CTG CAG ATG CTG GAG AAG CAG AAA AAG  //  GGC GGC GGT
```

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A [X]V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG [O]GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D

GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
CTG GCC GCC AGG GGC CGG GTC CAC CGG GGC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTC GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G K T E K T G K R S T S A A V L E A
GGC AAG ACG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC CTG GAG GCC

L R E A H P I V E K I L Q Y R E L T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K L K S T Y I D P L P D L I H P R T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G R L H T R F N Q T A T A T G R L S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

S S D P N L Q N I P V R T P L G Q R
AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

I R R A F I A E E G W L L V A L D Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S Q I E L R V L A H L S G D E N L I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R V F Q E G R D I H T E T A S W M F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G V P R E A V D P L M R R A A K T I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

N F G V L Y G M S A H R L S Q E L A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I P Y E E A Q A F I E R Y F Q S F P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K V R A W I E K T L E E G R R R G Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V E T L F G R R Y V P D L E A R V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

```

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

```

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein [Fig.17-GGG]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

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//
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// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein [Fig.17-HHH]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CAATTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITGGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGTG ATTACTTTGA AAAACATAGA TCITCCATAC 540
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TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
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CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTCG GGAAGAGAA 1560
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GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

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GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
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GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
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GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
ACAAACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC 2328
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ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

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Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein [Fig.17-III]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCGAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

Marked-Up Version

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GCAATTTTTT GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACCTGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTTCAAGGC AAGCACAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTTCGTT AAGAGGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATATCTCTT 1440
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GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTCG GGAAGAAGG 1560
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GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
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GAAGGAAAAG TCATTTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAAT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGATG ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC //

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// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

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Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein [Fig.17-JJJ]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)

Marked-Up Version

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTTAG GCTATTCCAA 60
AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCAATA CATTACGCT 120
CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
AAGATTGTGA GAAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
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CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAG AGCTAAAGAT TCCTGCCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
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AAAAAGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGCGATAT GACGGCTGAT GAAGTCAAGG GAAGATACA TTTCGACTTG 780
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TTATGGGATG TTTTCAAGGTG AAGCACAGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA 1080
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AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
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GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
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GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
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GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAATTTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTTAATT 2100

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TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC // 2328

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ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

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Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein [Fig.17-KKK]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71)

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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG AACTGACTA CATAACCGAG GATGGAAGC CTGTACATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CCGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
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GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTGCGCG AGGGGCCAAT CCTTATGATA 480
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GCCGCTCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
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CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
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CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTATGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260

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Marked-Up Version

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GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17.L.L

Sso7d - KOD DNA POLYMERASE fusion protein [Fig.17-L.LL]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

```

//ATGATCCTCG ACAC TGACTA CATAACCGAG GATGGAAAGC CTGTCAATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGACCAGTT 240
GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTTCG CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCAGCAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCCTTACCA TGAGGGCGAG GAGTTTCGCC AGGGCCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGG AGAACGTGGA TCTCCCTTAC 540
GTTGACGTCTG TCTCGACCGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
AAGCGTGTG AAAAGTCTGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCCTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTATGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCCG 1320
TTCTGCAAG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
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AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
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ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGGCTT CTTCTGTACG AAGAAGAAGT ATCGGTGAT AGACGAGGA 1800
GGCAAGATAA CAACCGCGCG ACTTGAGATT TGAAGCTTTG CTAAGGACG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CAGGGTTCT TGAAGCTTTG CGAAAAGCTG AGCAAGTAC AGGTTCCGCC GGAGAAGCTG 1920
AGGATAGTCA AGAAGTTTAC CGAAAAGCTG AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCAGACAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17- MMM]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

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ATGATACTGG ACACGTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
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CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAAATTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGACAAT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCCAAGATT AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTtaggaaa AACCaaaagc AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAActa GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCTTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
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Marked-Up Version

GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAATG AAATCCACAA TTGACCCGAT CGAAAGGAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTG CCGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGGCTT TAAGGTTCTT 1620
TATCGGGACA CTGACGGCTT TTTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGCTT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTGA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTCCACTT 1980
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CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN [Fig.17-NNN]

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAATTT GACCTCATTT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGTCTGA TGCAGTGAAA GTCCAGGAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTTAC GAATATGACA TACCTTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTTGAT TCCCATGGAG GGAGACGAGG AGCTTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGA AAAATATCGA TTTCCTGAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTATA 660
AAACGGGCAG AAAAGCTGGG AGTTCCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720

Marked-Up Version

CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
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 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAACA GCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCCTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC CTGATGAGGA AGAGTATAAA 1080
 AGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAAATACA TTTATTTTGA TTTCCGCGAGT CTGTACCCCTT CAATAATAAGT TACTCACAA 1260
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 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
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 AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
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 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATATA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCGGCGAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17000

Deep Vent- Ssod7 DNA polymerase fusion protein [Fig.17-000]

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCAGG GATGGGAAGC CGATTATAAG GATTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCCCTATATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTGAGGTTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATCTTT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAGC AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
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CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCCG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCA GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
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AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAACACAGT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGAGGGAA 1560
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GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCAG GGTGTGTGGA GCTTGATAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860

Marked-Up Version

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CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACGAGT ACAAGGCTAT AGTCCGCAC 2040
GTTGCCGTGG CAAAAGGTT AGCCGCTAGA GGAGTAAAG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCAATGGCTT AACATCAAGA AGAAG 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17PPP

Ssd7 - Deep Vent DNA polymerase fusion protein [Fig.17-PPP]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

```

```

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTCTGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300

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Marked-Up Version

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GACATAGAAA CCCTCTATCA CGAAGGGAG GAGTTCGGGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAAGCTGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCCAAAG 660
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TACCACGTGA TTAGGAGAAC GATAAAGCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGAG GACTGGAGAG AGTTGCAAAG TATTCATAGG AGGATGCAAA GGTAACGTAC 960
GAGTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
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GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCCG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTTCA GAGCCTGTAC CCCCTCGATA TAATCACCCA TAACGTCTCA 1260
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GAAGGGAAGA TAATCACATG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCC CTTACAGAGT ACAAGGCTAT AGTCCGCGAC 2040
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GGGTACATAG TGCTAGAGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA 2328

Figure 17RRR

Sso7d - JDF-3 fusion protein [Fig.17-RRR]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)


Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCAATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTGAAATACGACCGGAGTTCGAGCCCTACTTCT
 ACGGCTCCTCAGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGAGAGGACCGGAGGTCTGTTAAGTTAAGCGCGGAGAAAGTGAAGAAAAAGTTCTCTCGG
 CAGGTTCTGTGAGGTTCTGGTCTCTTACTTTCACGCAACCGCAGGACXXXCCGGCAATCCGGACAAATTAAGGAAGCACCCCGGTTCATCGACATCTACGAGTACGACATACCC
 TTCGCCAAGCGTACCTCATAGACAAGGCTTAATCCGATGGAAGAGCTTAACTCATGTCTTCCGATCGAGACGCTCTACCCAGGAGAACGAGTTGGAA
 CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGCGGTGATTAACCTGGAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
 GCGCTTCTTGAGGTCGTTAAGGAGAAGGACCCGACGTCTGATAACATACAAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
 ACCCTCGGAGGACGGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCTGAGGTGAAGGCGAGGTACCTTCGACCTTATCCAGTCTAAGGCGCACCATAA
 ACCTCCGACCTACACCTTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACGCCGAGGATAGCCACCGCTGGGAGACCGCGAGGGCTTGAGAG
 GGTCCGCGCTACTCGATGGAGGACGCGAGGTTTACCTACGAGCTTGGCAGGAGTCTTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGACGTTTCC
 CGTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCTACGAGAGGAACGAACCTCGTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
 ACgCGGTGGCTACGTCAAGGAGCGGAGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTCTAQCCTTCAATCATAATCACCCACAACGTCCTCGCAGATAC
 GCTCAACCGGAGGGGTGATAGGAGCTACGACGTTGCCCCGAGGTCCGTCAACAAGTTCTGCAAGGACTTCCCGGCTTCAATCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGG
 CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
 ATGCCAGGGCAAGATGGTACTCGAGGAGTGC CGCGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCTATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCTCT
 CTATGCAGACACAGACGGTCTCCATGCCACCACTTCTGGAGCGGACGCTGAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGCTTCTC
 GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTACGAAGAAAAAGTACCGGTCTATCGACGAGAGGGCAAGATAACACCGCGGGCTTGAGATAGTACGAGCGG
 ACTGGAGCGGATAGCGAAGGAGACGCGAGCGAGGTTTGGAGCGGATATCTAGGCAACGTTGAGAGGCCCTCAGAAATTGTACGGGAAGTCAACCGAAAAAGCTGAGCAA
 GTACGAGGTTCCGCGGAGAAAGCTGTGTTATCCACGAGCAGATTAACCGCGGAGCTCAAGGACTACAAAGCCACCGGCCGACGTAGCCATAGCGAAgCGTTTGGCCCGCAGGAT
 GTTAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCAAGTACGATG
 CGGACTACTACATCGAAGAACGAGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCTTCGGCTACCGAAGACGAGGCAAGTTCGGGCTTGGCGC
 GTGGCTGAAGCCGAAGGGGAAGAAGTGA

a

MkTpV 1 valvydaefvgsererefeetflkcvkaydgvlattylmersssaandelllelhq
 RecA VI cgnalkfyasvrlldirrlgaidgdEvvg
 MkTpV 179 vppdekeertrleirenpwtphdrlarrgGLSVSevegekdpessgiyslwsrvvvv
 HTH asnC tprldrkrtnepqkdgRRISnrlakrvGLSVStvrervrr
 HTH SS 

b

[illegible]

FIGURE 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020))

FIGURE 19

[Fig. 19]

SEQ ID NO: 120 **Synthetic Sso7d gene**

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 **The amino acid sequence of Sso7d.**

ATVKFKYKGEEKEVDISKIKVWRVGMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 **The DNA sequence encoding the Sso7d-ΔTaq fusion protein**

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGCTACTAGTCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCGCGGAAGGGGCC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCTTTCCGCTGTCCTGGCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
GGACCAGCTGGAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGTCCACCAGCGCCGCTCCTGGAGGCCCTCCG
CGAGGCCCAACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCCGTCCGCAACCCGCTTGGGCAGAGGATCCCG
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGGCGTCC
CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCTCTACGGCATGTCGGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC
CCTCTTCGGCCGCCGCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTA A

SEQ ID NO: 123 **The amino acid sequence of Sso7d-ΔTaq fusion protein**

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA
ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHLRSQELAIPIYEEAQAFIERYFQSFVKVRAWIEKTLEEGRRRRGYVETLFGRR
RYVPDLEARVKSVEAERMAFNMPVQGTAAADLMKLAMVKLFPRL EEMGARMLL
QVHDELVL EAPKERA EAVARLAKEVM EGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCAGTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGTCTCTCTGGTG
GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCCACGCCAG
AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
GGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCTTGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCTCACC GCCGACAAAG
ACCTTTACAGCTCCTTTCCGACCGCATCCACGTCTCTCACC CCGAGGGGTACCT
CATCACC CCGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCA GTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
GAAAGCCCCAAGGCCTGGAGGAGGCCCCCTGGCCCCGCGGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCT
CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTACCGGGAGGT
GGAGAGGCCCTTTCCGCTGTCTTGCCCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCTTGAGGTGGCCGAGGAGATCGCCCCG
CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCCGCGTCTTGAGGGCCCTCCGC
GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTACCAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCACC CAGGACGGGCGGCC
TCCACACC CCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGTCAAGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGCGTCCCC

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CGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTCGGCCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTAGAGCTTCCCCAAGGTGCGGGC
CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCCCGCCGCTACGTGCCAGACCTAGAGGCCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCC
TGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGCGGAGGCGGGCATCATCATCATCATTA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSGLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFAXSLLKALKEDGDAVIVVFDKAPSRHEAYGGYKAGRPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLSDR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKARKLL
EEWGSLEALLKNLDRCLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLEFLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQIRJRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHLRSQELAIPEYEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETL
FGRRRYVPDLERVKSVREAAERMAFNMPVQGTAAADLMKLAAMVKLFPRLEEMGA
RMLLQVHDELVLAPKERAEEAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHHH

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTATAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTTCGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAACTTGGGATTAAATTAACCATTTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTCT
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAGAAACGAAGTAGTCTCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG

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CTCAGGGAGAGCTACACAGGTGGATTTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC
TTGGGACATTTGTTAGAGGAAAAGACAAAAGATTAAAGACAAAAATGAAGGAACT
TTAGCAAATTCCTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG
GTCTCTATGCAACTATCCCAGGAGGAGAAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
GAGTGAAATTGCAAAAAGAACTCAAGCTAGAGTTTTGGAGACAATACTAAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAACTAGCT
GCTAAAGGAGTTAAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCCAAA
AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGATTGGATACAGAAAGGAAGACCTCAGATACCAAAAAG
ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAATAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID
LPYVEVVSSEREMIKRFLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI
AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESYTGGFVKEPEKGLWENIVYLDLR
ALYPSIIHTNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYE
GFYKRGFFVTKKRYAVIDEKGKVTIRGLEIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
MVGIVYVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
LRYQKTRQVGLTSWLNKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

atgattacga	attcgacggt	gaaggtaaag	ttcaagtata	aggggtgaaga	gaaagaagta
gacacttcaa	agataaagaa	ggtttggaga	gtaggcaaaa	tgggtgcctt	tacctatgac
gacaatggta	agacaggttag	aggagctgta	agcgagaaaag	atgctccaaa	agaattatta
gacatgtag	caagagcaga	aagagagaag	aaaggcggcg	gtgtcactag	ccccaaggcc
ctggaggagg	ccccctggcc	cccgccggaa	ggggccttcg	tgggctttgt	gctttcccg
aaggagccca	tgtgggccga	tcttctggcc	ctggccggcg	ccaggggggg	ccgggtccac
cgggcccccg	agccttataa	agccctcagg	gacctgaagg	aggcgcgggg	gcttctcgcc
aaagacctga	gcgttctggc	cctgagggaa	ggccttggcc	tcccgcccg	cgacgacccc
atgctcctcg	cctacctcct	ggacccttcc	aacaccaccc	ccgagggggg	ggcccgggcg
tacggcgggg	agtggacgga	ggaggcgggg	gagcggggcg	ccctttccga	gaggctcttc
gccaacctgt	gggggaggct	tgagggggag	gagaggctcc	tttggcttta	ccgggagggtg

Marked Up Version

gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg
gcctatctca gggccttgtc cctggagtg gccgaggaga tcgccgcct cgaggccgag
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc
ctctttgacg agctagggtt tcccgccatc ggcaagacgg agaagaccgg caagcgctcc
accagcgccg ccgtcctgga ggccctccgc gagggcccacc ccatcgtgga gaagatcctg
cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc
caccacagga cgggcgcgct ccacaccgcg ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg
atccgcccgg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttcag
gaggggcccg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc
gtggaccccc tgatgcgcgc ggccggcaag accatcaact tcggggtcct ctacggcatg
tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca gcccttcatt
gagcgctact ttcagagctt ccccaaggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta
gagggcccgg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
cagggcaccg ccgcccacgt catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggtc cagcagcagc tggtcctcga ggcacaaaa
gagagggcgg agggcgtggc ccggctggcc aaggaggtca tggagggggg gtatccctg
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa

SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGMVSFTYDDNGKTGRGAVSEKDA
PKELLDMLARAEREKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
DPSNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI
HPRTGRLHTRFNQTATATGRLSSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDY
SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
VLYGMSAHLRSQELAIPIYEEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFR
RRYVPDLEARVKSAREMAAFNMPVQGTAAADLMKLMVKLFPRLEEMGARMML
LQVHDELVLEAPKERAEEAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKEGIDG
RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
GCAAGATGATCTCCTTACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG
CGGTAAGCGAAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
AAAAAGGGCGGCGGTGTACCAAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
CCGCCGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
CCGATCTTCTGGCCCTGGCCGCCGAGGGGGGGCCGGGTCCACCGGGCCCCCG
AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG
ACCTGAGCGTCTTGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
CATGCTCCTCGCTACCTCCTGACCTTCCAACACCAACCCCGAGGGGGTGGCC
CGGCGCTACGCGGGGAGTGGACGAGGAGGCGGGGGAGCGGGCCGCCCTTTCC
GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCTTTCCGCTGTCCTGGCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
AACCTCAACTCCCGGGACCAAGCTGGAAAGGCTCCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGAGAGAACCGGCAAGCGCTCCACCAGCGCCCGCGTCC
TGGAGGCCCTCCGCGAGGCCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGG

AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG
ATGTTTCGGCGTCCCCCGGGAGGCGGTGGACCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGGTCTCTACGGCATGTGCGCCACCGCCTCTCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCCGTACGTGCCAGACCTAGAGGCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCC
AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
ATCATCATATTAA

SEQ ID NO: 131 **The amino acid sequence of PL-ΔTaq fusion protein**

MITNSKKKKKKRKRKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLDFDELGLPAIGKTEKTGKRSTSAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLDLHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDNLRVVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVL YGMSAHRLSQELAIPEYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKS VREAAERMAFNMVPVQGTAA
LMKLAMVKLFPRL EEMGARMLLQVHDELVLEAPKERA EAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 **PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'**

SEQ ID NO: 133 **PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'**

SEQ ID NO: 134 **PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'**

SEQ ID NO: 135 **PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'**

SEQ ID NO: 136 **PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'**

SEQ ID NO: 137 **PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'**

SEQ ID NO: 138 **PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'**

SEQ ID NO: 139 **PRIMER L3512IR 30 5'- CACATGGTACAGCAAGCCTGGC-3'**

SEQ ID NO: 140 **PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'**

SEQ ID NO: 141 **PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'**

SEQ ID NO: 142 **PRIMER L3035OF 5 5'-CCTGCCTGCCGCTTCACGC-3'**

Marked Up Version

SEQ ID NO: 143 **PRIMER L40547R** 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 **PRIMER H-Amelo-Y** 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 **PRIMER H-Amelo-YR** 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 **Human beta-globin primer 536F** 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 **Human beta-globin primer 536R** 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 **Human beta-globin primer 1408R** 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

MARKED UP VERSION OF AMENDED FIGURE 20

Please replace Figure 20 with the replacement Figure below, which is marked up by way of bracketing and **DOUBLE** underlining to show the changes relative to the previous version of Figure 20.

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile

Marked-Up Version

165					170					175					
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys
			180					185					190		
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr
		195					200					205			
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu
	210					215					220				
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys
225						230					235				240
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile
			245						250					255	
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr
		260						265					270		
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu
		275					280					285			
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Ser	Gly	Glu	Asn
	290					295					300				
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr
305						310					315				320
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu
			325						330					335	
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu
			340					345					350		
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala
	355						360					365			
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser
	370					375					380				

Marked-Up Version

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
 385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
 405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
 420 425 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
 435 440 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
 450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
 465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
 485 490 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
 500 505 510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
 515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
 530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
 545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 580 585 590

Marked-Up Version

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625 630 635 640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
740 745 750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
755 760 765

Trp Leu Asn Ile Lys Lys Ser
770 775

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

Marked-Up Version

ccctggctcct ggggtccacat atatgttctt actcgctttt atgaagaatc cccagtcgc	60
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat	120
caactctaca cctcccctat tttctctctt atgagatfff taagtatagt tatagagaag	180
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga	240
ttacataact gaagaaggaa aacctgttat taggctattc aaaaagaga acggaaaatt	300
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc	360
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt	420
tgatgtagag aagggtgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta	480
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt	540
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct	600
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta	660
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa	720
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag	780
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat	840
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact	900
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga	960
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag	1020
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc	1080
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga	1140
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt	1200
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag	1260
gtcaagcaca gggaaccttg tagagtgggtt cttacttagg aaagcctacg aaagaaacga	1320
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac	1380
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt	1440
tagagcccta tatccctcga ttataattac ccacaatggt tctcccgata ctctaaatct	1500
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat	1560

ccctggtttt	ataccaagtc	tcttgggaca	tttgtttagag	gaaagacaaa	agattaagac	1620
aaaaatgaag	gaaactcaag	atcctataga	aaaaatactc	cttgactata	gacaaaaagc	1680
gataaaactc	ttagcaaatt	ctttctacgg	atattatggc	tatgcaaaag	caagatggta	1740
ctgtaaggag	tgtgctgaga	gcgttactgc	ctggggaaga	aagtacatcg	agttagtatg	1800
gaaggagctc	gaagaaaagt	ttggatttaa	agtcctctac	attgacactg	atggctctcta	1860
tgcaactatc	ccaggaggag	aaagtgagga	aataaagaaa	aaggctctag	aatttgtaaa	1920
atacataaat	tcaaagctcc	ctggactgct	agagcttgaa	tatgaagggg	tttataagag	1980
gggattcttc	gttacgaaga	agaggatatgc	agtaatagat	gaagaaggaa	aagtcattac	2040
tcgtggttta	gagatagtta	ggagagattg	gagtgaatt	gcaaaagaaa	ctcaagctag	2100
agttttggag	acaatactaa	aacacggaga	tgttgaagaa	gctgtgagaa	tagtaaaaga	2160
agtaatacaa	aagcttgcca	attatgaaat	tccaccagag	aagctcgcaa	tatatgagca	2220
gataacaaga	ccattacatg	agtataaggc	gataggctcct	cacgtagctg	ttgcaaagaa	2280
actagctgct	aaaggagtta	aaataaagcc	aggaatggta	attggataca	tagtacttag	2340
aggcgatgg	ccaattagca	atagggcaat	tctagctgag	gaatacgatc	ccaaaaagca	2400
caagtatgac	gcagaatatt	acattgagaa	ccaggttctt	ccagcggtac	ttaggatatt	2460
ggagggattt	ggatacagaa	aggaagacct	cagataccaa	aagacaagac	aagtcggcct	2520
aacttcttgg	cttaacatta	aaaaatccta	gaaaagcgat	agatatcaac	ttttattctt	2580
tctaaccctt	ttctatgaaa	gaagaactga	gcaggaatta	ccagttcttc	cgttatttta	2640
tgggtaatta	aaaacccatg	ctcttgggag	aatcttcgaa	taaaatccct	aacttcaggc	2700
tttgctaagt	gaatagaata	aacaacatca	ctcacttcaa	acgccttcgt	tagaaatgg	2760
ctatctgcat	gcttctctgg	ctcggaann	gaggattcat	aacaacagta	tcaacattct	2820
cagagaattg	agaaacatca	gaaactttga	cttctacaac	atctctaact	ttgcaactct	2880
tcaagatttt	ctaaaagaat	tttaacggcc	tcctcgtaaa	tttcgacgac	gtagatcttt	2940
tttgctccaa	gcagagccgc	tccaatggat	aacacccctg	ttcccgcacc	caagtccgct	3000
acaatttttt	ccttgatatc	cctaattgtat	aagcaagcca	aaggagagta	gatgctacct	3060
ttccgggagt	tttgatttgc	tctagccaag	gtttgggatt	tttgaatcct	ttaactctgg	3120
aaagtataat	ttcaagctcc	ttcttcttca	tgacagatga	aaaattggtt	tgtctctttt	3180

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta	3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc	3300
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtggt cagactttta	3360
gacactcaaa taccagacga caatggtgtg ctactcaag ccccatatgg gttgagaaaa	3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga	3480
aagattgaga tgttcttgg	3499